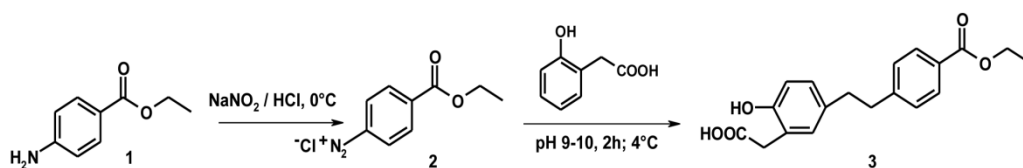
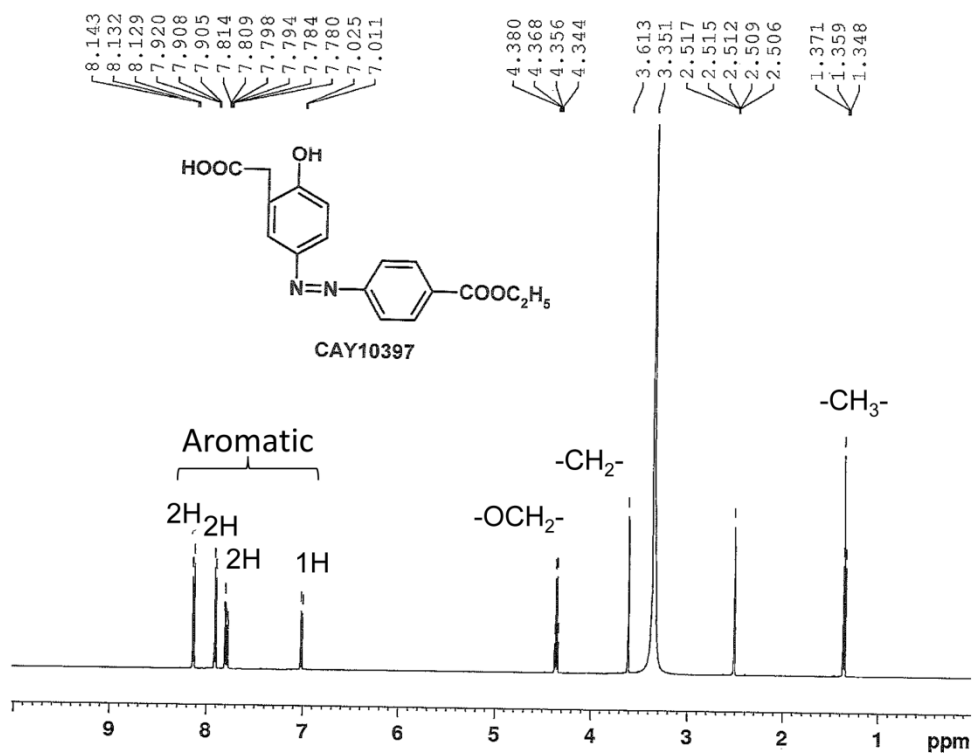


SUPPLEMENTARY DATA

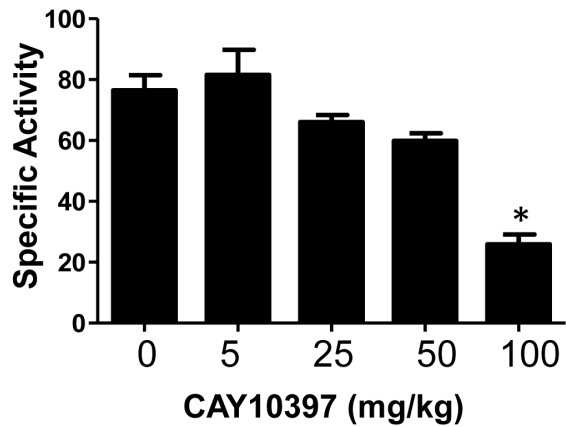
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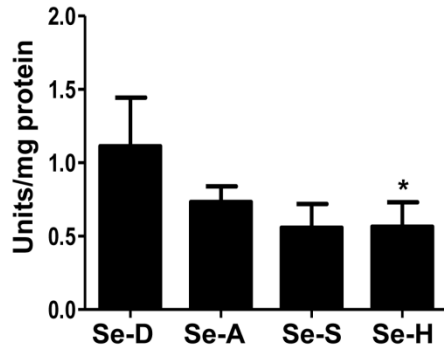
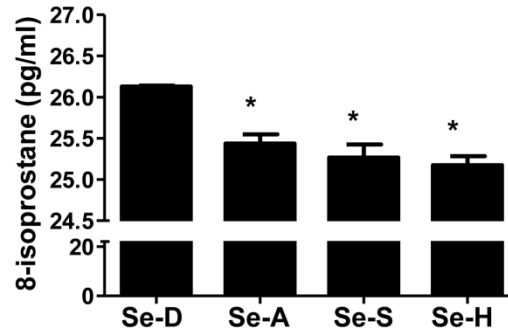
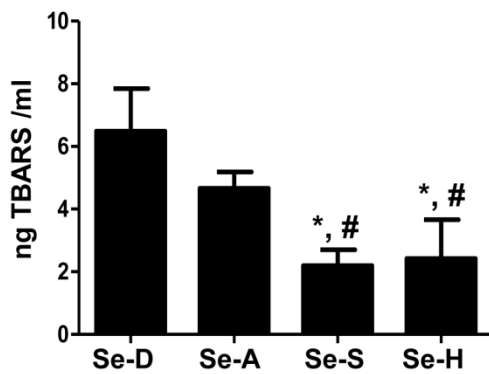
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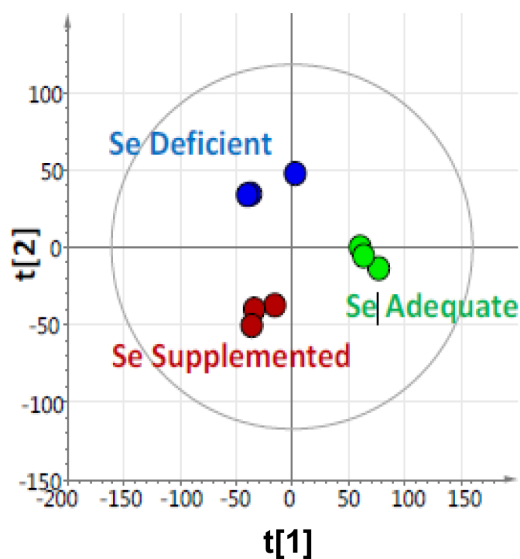
Supplementary Figure 1 (A) Chemical synthesis scheme for CAY10397. **(B)** ¹H-NMR of purified CAY10397.



Supplementary Figure 2 Inhibition of 15-PGDH activity in the kidney extracts of mice treated with increasing doses of CAY10397 by oral gavage. C57BL/6 mice were orally gavaged every alternate day with 5-100 mg/kg CAY10397 formulated in 20 mM glycine buffer (pH 10) with 5 % (v/v) DMSO for 10 days. Kidney extracts were prepared and cytoplasmic fractions were used for the 15-PGDH enzyme assay as described earlier. All data shown are mean \pm SEM on n=3 per group.

A**B****C**

Supplementary Figure 3 Inverse causal relationship between oxidative stress markers in the colon and Se status of DSS-treated mice. Colonic extracts from DSS-treated mice on day 10 were prepared and used in assays to examine the levels of (A) myeloperoxidase (MPO) activity, (B) 8-isoprostane (8-iso-PGF_{2α}), and (C) lipid peroxidation. All data shown are mean ± SEM on n=3 per group. p<0.05 compared to Se-D group.



Supplementary Figure 4 Principal component analysis of metabolites as a function of Se status of mice. Twenty four hour pooled urine samples (~ 20 µl) from Se-D, Se-A, and Se-S mice (before treatment with DSS) were collected, deproteinized overnight with 100 µl of aqueous acetonitrile (50 %) at -20 °C. The samples were centrifuged, dried in a speed-vac system, and resuspended in 100 µl of 1 µM chlorpropamide (as internal standard) solution (in water). These samples were subjected to mass spectrophotometry. The spectral data was deconvoluted using MarkerLynx software program (Waters). The characteristics such as m/z , retention time, peak area of each data point were analyzed. PCA (principal components analysis) and PLS-DA (supervised projection to latent structures-discriminant analysis) were conducted using SIMCA P12+ software (Umetrics). Candidate biomarkers were searched using the METLIN (metabolite and tandem MS database) database. n= 3 mice per group.